REMARKS

Claims 1-73 were originally filed with the application. By amendment herein, claims 8, 9 and 37-39 have been canceled, without prejudice or disclaimer. Dependent claim 40 has been amended to independent form in order to make explicit what was previously implicit in this claim. (See, also original claims 34 and 37). Claims 34, 44, 65, 67, 72 and 73 have been amended to correct antecedent basis and for clarity. Entry of the foregoing amendments is respectfully requested prior to substantive examination. Thus, claims 1-7, 10-36, and 40- 73 are under consideration.

Applicants also attach hereto their requests for corrected filing receipts (mailed on March 25, 2002 and faxed on April 4, 2003) as well as a status inquiry regarding the March 25, 2002 request for a corrected filing receipt (mailed on October 28, 2002). The correct filing date of this application is October 24, 2001.

Respectfully submitted,

Date: 9 April 03

By: Dfasternak

Dahna S. Pasternak
Registration No. 41,411
Attorney for Applicants

Cooley Godward LLP
Five Palo Alto Square
3000 El Camino Real
Palo Alto, CA 94306
Tel.: (650) 843-5608
Fax: (650) 857-0663

Version Showing Changes Made to Claims

Claims 8, 9, and 37-39, have been canceled, without prejudice or disclaimer.

Claims 1, 34, 40, 44, 65, 67, 72 and 73 are amended as follows:

1. (Amended) A method for modifying a region of interest in cellular chromatin, the method comprising the step of contacting the cellular chromatin with [a] the fusion molecule [that binds to a binding site in the region of interest, wherein the fusion molecule comprises a DNA binding domain and a component of a chromatin remodeling complex or functional fragment thereof] according to claim 40, thereby modifying the region of interest.

34. (Amended) The fusion molecule of claim 40, wherein said molecule is a fusion polypeptide. [A fusion polypeptide comprising:

a) a DNA binding domain; and

b) a component of a chromatin remodeling complex or a functional fragment thereof].

40. (Amended) [The] A fusion molecule comprising:

a) a DNA binding domain; and

b) an enzymatic component of a chromatin remodeling complex or a functional fragment thereof [polypeptide of claim 37], wherein the enzymatic component of a chromatin remodeling complex or functional fragment thereof is selected from the group consisting of a histone methyl transferase, a histone demethylase, a histone kinase, a histone phosphatase, a histone ubiquitinating enzyme, a histone-ADP-ribosylase and a histone protease.

44. (Amended) A method for modulating expression of a gene, the method comprising the steps of:

a) contacting cellular chromatin with [a first] the fusion molecule [that binds to a binding site in cellular chromatin, wherein the binding site is in the gene and wherein the first fusion molecule comprises a DNA-binding domain and a component of a chromatin remodeling complex or functional fragment thereof] according to claim 40; and

b) further contacting the cellular chromatin with a second molecule that binds to a target site in the gene and modulates expression of the gene.

65. (Amended) The method of claim 60 wherein the first fusion molecule binds to [a

shared binding site in] two or more of the plurality of genes.

67. (Amended) The method of claim 60 wherein the second molecule binds to [a shared target site in] two or more of the plurality of genes.

72. (Amended) A method for producing [a] the fusion polypeptide of claim 34, [wherein the fusion polypeptide comprises a zinc finger DNA binding domain and a component of a chromatin remodeling complex or a functional fragment thereof,] the method comprising the step of expressing the polynucleotide of claim 41 in a suitable host cell.

73. (Amended) A method for binding an exogenous molecule to a binding site, wherein the binding site is located within a region of interest in cellular chromatin, wherein the method comprises:

(a) contacting cellular chromatin with a fusion molecule according to claim 40 [that binds to a binding site in the region of interest, wherein the fusion molecule comprises a DNA binding domain and a component of a chromatin remodeling complex or functional fragment thereof, thereby modifying cellular chromatin within the region of interest]; and

(b) introducing the exogenous molecule into the cell;

whereby the exogenous molecule binds to the binding site.

Currently Pending Claims

1. (Amended) A method for modifying a region of interest in cellular chromatin, the method comprising the step of contacting the cellular chromatin with the fusion molecule according to claim 40, thereby modifying the region of interest.

2. The method of claim 1, wherein the cellular chromatin is present in a plant cell.

3. The method of claim 1, wherein the cellular chromatin is present in an animal cell.

4. The method of claim 3, wherein the cell is a human cell.

5. The method of claim 1, wherein the fusion molecule is a fusion polypeptide.

6. The method of claim 1, wherein the DNA-binding domain comprises a zinc finger DNA-binding domain.

7. The method of claim 1, wherein the DNA-binding domain is a triplex-forming nucleic acid or a minor groove binder.

8. *Canceled.*

9. *Canceled.*

10. The method of claim 1, wherein chromatin modification facilitates detection of a sequence of interest.

11. The method of claim 10, wherein the sequence of interest comprises a single nucleotide polymorphism.

12. The method of claim 1, wherein chromatin modification facilitates activation of a gene of interest.

13. The method of claim 1, wherein chromatin modification facilitates repression of a

gene of interest.

14. The method of claim 1, wherein chromatin modification facilitates recombination between an exogenous nucleic acid and cellular chromatin.

15. The method of claim 5, wherein the method further comprises the step of contacting a cell with a polynucleotide encoding the fusion polypeptide, wherein the fusion polypeptide is expressed in the cell.

16. The method of claim 1, further comprising the step of identifying an accessible region in the cellular chromatin, wherein the fusion molecule binds to a target site in the accessible region.

17. The method of claim 1, wherein the region of interest comprises a gene.

18. The method of claim 17, wherein the gene encodes a product selected from the group consisting of vascular endothelial growth factor, erythropoietin, androgen receptor, PPAR-γ2, p16, p53, pRb, dystrophin and e-cadherin.

19. The method of claim 1, further comprising the step of contacting the cellular chromatin with a second molecule.

20. The method of claim 19, wherein the second molecule is a transcriptional regulatory protein.

21. The method of claim 19, wherein the second molecule is a fusion molecule.

22. The method of claim 21, wherein the second molecule is a fusion polypeptide.

23. The method of claim 21, wherein the second molecule comprises a zinc finger DNA-binding domain.

24. The method of claim 23, wherein the second molecule further comprises a transcriptional activation domain.

25. The method of claim 23, wherein the second molecule further comprises a transcriptional repression domain.

26. The method of claim 23, wherein the second molecule further comprises a polypeptide sequence selected from the group consisting of a histone acetyl transferase, a histone deacetylase, a functional fragment of a histone acetyl transferase, and a functional fragment of a histone deacetylase.

27. The method of claim 19, further comprising the step of contacting the cellular chromatin with a third molecule.

28. The method of claim 27, wherein the third molecule is a transcriptional regulatory protein.

29. The method of claim 27,wherein the third molecule is a fusion molecule.

30. The method of claim 29,wherein the third molecule is a fusion polypeptide.

31. The method of claim 29, wherein the third molecule comprises a zinc finger DNA-binding domain.

32. The method of claim 31, wherein the third molecule further comprises a transcriptional activation domain.

33. The method of claim 31, wherein the third molecule further comprises a transcriptional repression domain.

34. (Amended) The fusion molecule of claim 40, wherein said molecule is a fusion polypeptide.

35. The polypeptide of claim 34, wherein the DNA-binding domain is a zinc finger DNA binding domain.

36. The polypeptide of claim 34, wherein the DNA binding domain binds to a target site in a gene encoding a product selected from the group consisting of vascular endothelial growth factor, erythropoietin, androgen receptor, PPAR-γ2, p16, p53, pRb, dystrophin and e-cadherin.

37 through 39. *Canceled.*

40. (Amended) A fusion molecule comprising:

a) a DNA binding domain; and

b) an enzymatic component of a chromatin remodeling complex or a functional fragment thereof, wherein the enzymatic component of a chromatin remodeling complex or functional fragment thereof is selected from the group consisting of a histone methyl transferase, a histone demethylase, a histone kinase, a histone phosphatase, a histone ubiquitinating enzyme, a histone-ADP-ribosylase and a histone protease.

41. A polynucleotide encoding the fusion polypeptide of claim 34.

42. A cell comprising the fusion molecule of claim 34.

43. A cell comprising the polynucleotide of claim 41.

44. (Amended) A method for modulating expression of a gene, the method comprising the steps of:

a) contacting cellular chromatin with the fusion molecule according to claim 40; and

b) further contacting the cellular chromatin with a second molecule that binds to a target site in the gene and modulates expression of the gene.

45. The method of claim 44, wherein modulation comprises activation of expression of the gene.

46. The method of claim 44, wherein modulation comprises repression of expression of the gene.

47. The method of claim 44 wherein the DNA-binding domain of the first fusion molecule comprises a zinc finger DNA-binding domain.

48. The method of claim 44 wherein the second molecule is a polypeptide.

49. The method of claim 48 wherein the second molecule comprises a zinc finger DNA-binding domain.

50. The method of claim 49, wherein the second molecule further comprises an activation domain.

51. The method of claim 49, wherein the second molecule further comprises a repression domain.

52. The method of claim 44 wherein the second molecule is a transcription factor.

53. The method of claim 52 wherein the transcription factor is an exogenous molecule.

54. The method of claim 52 wherein the transcription factor is an endogenous molecule.

55. The method of claim 44 wherein the first fusion molecule and the second molecule each comprise a zinc finger DNA-binding domain.

56. The method of claim 44 wherein a plurality of first fusion molecules is contacted with cellular chromatin, wherein each of the first fusion molecules binds to a distinct binding site.

57. The method of claim 44, wherein a plurality of second molecules is contacted with cellular chromatin, wherein each of the second molecules binds to a distinct target site.

58. The method of claim 56 wherein at least one of the first fusion molecules comprises a zinc finger DNA-binding domain.

59. The method of claim 57 wherein at least one of the second molecules comprises a zinc finger DNA-binding domain.

60. The method of claim 44 wherein the expression of a plurality of genes is modulated.

61. The method of claim 60 wherein a plurality of first fusion molecules is contacted with cellular chromatin, wherein each of the first fusion molecules binds to a distinct binding site.

62. The method of claim 61 wherein at least one of the first fusion molecules is a zinc finger fusion polypeptide.

63. The method of claim 60, wherein a plurality of second molecules is contacted with cellular chromatin, wherein each of the second molecules binds to a distinct binding site.

64. The method of claim 63 wherein at least one of the second molecules is a zinc finger fusion polypeptide.

65. (Amended) The method of claim 60 wherein the first fusion molecule binds to two or more of the plurality of genes.

66. The method of claim 65 wherein the first fusion molecule is a zinc finger fusion polypeptide.

67. (Amended) The method of claim 60 wherein the second molecule binds two or more of the plurality of genes.

68. The method of claim 67 wherein the second molecule is a zinc finger fusion polypeptide.

69. The method of claim 1, wherein chromatin modification results in the generation of an accessible region in the cellular chromatin.

70. The method of claim 69, wherein generation of the accessible region facilitates binding of an exogenous molecule.

71. The method of claim 70, wherein the exogenous molecule is selected from the group

consisting of polypeptides, nucleic acids, small molecule therapeutics, minor groove binders, major groove binders and intercalators.

72. (Amended) A method for producing the fusion polypeptide of claim 34, the method comprising the step of expressing the polynucleotide of claim 41 in a suitable host cell.

73. (Amended) A method for binding an exogenous molecule to a binding site, wherein the binding site is located within a region of interest in cellular chromatin, wherein the method comprises:

(a) contacting cellular chromatin with a fusion molecule according to claim 40; and

(b) introducing the exogenous molecule into the cell;

whereby the exogenous molecule binds to the binding site.